

SEQUENCE LISTING

<110> Novozymes A/S
Thisted, Thomas
Kjaerulff, Soren
Andersen, Carsten
Fuglsang, Claus Crone

<120> Alpha-amylase mutants with altered properties

<130> 10062.200-US

<140> To Be Assigned

<141> 2001-07-31

<160> 30

<170> PatentIn version 3.2

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<211> 1455

<212> DNA

<213> Bacillus sp.

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Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala	
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aac tta aag agt aaa ggg ata aca gct gta tgg atc cca cct gca tgg	144
Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp	
35 40 45	
aag ggg act tcc cag aat gat gta ggt tat gga gcc tat gat tta tat	192
Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr	
50 55 60	
gat ctt gga gag ttt aac cag aag ggg acg gtt cgt aca aaa tat gga	240
Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly	
65 70 75 80	
aca cgc aac cag cta cag gct gcg gtg acc tct tta aaa aat aac ggc	288
Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly	
85 90 95	
att cag gta tat ggt gat gtc gtc atg aat cat aaa ggt gga gca gat	336
Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp	
100 105 110	

ggt acg gaa att gta aat gcg gta gaa gtg aat cgg agc aac cga aac Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn 115 120 125	384
cag gaa acc tca gga gag tat gca ata gaa gcg tgg aca aag ttt gat Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp 130 135 140	432
ttt cct gga aga gga aat aac cat tcc agc ttt aag tgg cgc tgg tat Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr 145 150 155 160	480
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ata tat aaa ttc agg gga aca ggc aag gcc tgg gac tgg gaa gtc gat Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp 180 185 190	576
aca gag aat ggc aac tat gac tat ctt atg tat gca gac gtg gat atg Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met 195 200 205	624
gat cac cca gaa gta ata cat gaa ctt aga aac tgg gga gtg tgg tat Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr 210 215 220	672
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ata aaa tat agc ttt acg aga gat tgg ctt aca cat gtg cgt aac acc Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr 245 250 255	768
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340 345 350	
tat gca ttg gtt ctg aca agg gaa caa ggt tat cct tcc gta ttt tat	1104
Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr	
355 360 365	
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Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser	
370 375 380	
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Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr	
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Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu	
405 410 415	
gga aat agc tcc cat cca aat tca ggc ctt gcc acc att atg tca gat	1296
Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp	
420 425 430	
ggt cca ggt ggt aac aaa tgg atg tat gtg ggg aaa aat aaa gcg gga	1344
Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly	
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Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile	
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Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp	

35

40

45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
 50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
 65 70 75 80

Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
 85 90 95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
 100 105 110

Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
 115 120 125

Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
 130 135 140

Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
 145 150 155 160

His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
 165 170 175

Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
 180 185 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
 195 200 205

Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr
 210 215 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
 225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
 245 250 255

Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
 260 265 270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
 275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
 290 295 300

Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
 305 310 315 320

His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
 325 330 335

Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala
 340 345 350

Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
 355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
 370 375 380

Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr
 385 390 395 400

Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
 405 410 415

Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
 420 425 430

Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly
 435 440 445

Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
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Val Trp Val Lys Gln
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 ttg cct aat gat ggg aat cac tgg aat aga tta aga gat gat gct agt 96
 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser
 20 25 30
 aat cta aga aat aga ggt ata acc gct att tgg att ccg cct gcc tgg 144
 Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp
 35 40 45
 aaa ggg act tcg caa aat gat gtg ggg tat gga gcc tat gat ctt tat 192
 Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
 50 55 60
 gat tta ggg gaa ttt aat caa aag ggg acg gtt cgt act aag tat ggg 240
 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
 65 70 75 80
 aca cgt agt caa ttg gag tct gcc atc cat gct tta aag aat aat ggc 288
 Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly
 85 90 95
 gtt caa gtt tat ggg gat gta gtg atg aac cat aaa gga gga gct gat 336
 Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
 100 105 110
 gct aca gaa aac gtt ctt gct gtc gag gtg aat cca aat aac cgg aat 384
 Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn
 115 120 125
 caa gaa ata tct ggg gac tac aca att gag gct tgg act aag ttt gat 432
 Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
 130 135 140
 ttt cca ggg agg ggt aat aca tac tca gac ttt aaa tgg cgt tgg tat 480
 Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr
 145 150 155 160
 cat ttc gat ggt gta gat tgg gat caa tca cga caa ttc caa aat cgt 528
 His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg
 165 170 175
 atc tac aaa ttc cga ggt gat ggt aag gca tgg gat tgg gaa gta gat 576

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			180					185					190				
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Ser	Glu	Asn	Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Val	Asp	Met		
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Asp	His	Pro	Glu	Val	Val	Asn	Glu	Leu	Arg	Arg	Trp	Gly	Glu	Trp	Tyr		
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Thr	Asn	Thr	Leu	Asn	Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Val	Lys	His		
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Ile	Lys	Tyr	Ser	Phe	Thr	Arg	Asp	Trp	Leu	Thr	His	Val	Arg	Asn	Ala		
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acg	gga	aaa	gaa	atg	ttt	gct	gtt	gct	gaa	ttt	tgg	aaa	aat	gat	tta	816	
Thr	Gly	Lys	Glu	Met	Phe	Ala	Val	Ala	Glu	Phe	Trp	Lys	Asn	Asp	Leu		
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Gly	Ala	Leu	Glu	Asn	Tyr	Leu	Asn	Lys	Thr	Asn	Trp	Asn	His	Ser	Val		
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Phe	Asp	Val	Pro	Leu	His	Tyr	Asn	Leu	Tyr	Asn	Ala	Ser	Asn	Ser	Gly		
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Gly	Asn	Tyr	Asp	Met	Ala	Lys	Leu	Leu	Asn	Gly	Thr	Val	Val	Gln	Lys		
305					310					315					320		
cat	cca	atg	cat	gcc	gta	act	ttt	gtg	gat	aat	cac	gat	tct	caa	cct	1008	
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Tyr	Ala	Leu	Ile	Leu	Thr	Arg	Glu	Gln	Gly	Tyr	Pro	Ser	Val	Phe	Tyr		
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Gly	Asp	Tyr	Tyr	Gly	Ile	Pro	Thr	His	Ser	Val	Pro	Ala	Met	Lys	Ala		
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aat	gca	gat	gga	tgg	gct	aat	ttt	tca	gta	aat	gga	gga	tct	gtt	tcc	1440				
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att	tgg	gtg	aaa	cga											1455					
Ile	Trp	Val	Lys	Arg																
485																				

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Val	Gln	Val	Tyr	Gly	Asp	Val	Val	Met	Asn	His	Lys	Gly	Gly	Ala	Asp
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Ala	Thr	Glu	Asn	Val	Leu	Ala	Val	Glu	Val	Asn	Pro	Asn	Asn	Arg	Asn		
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Asp	His	Pro	Glu	Val	Val	Asn	Glu	Leu	Arg	Arg	Trp	Gly	Glu	Trp	Tyr		
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Thr	Asn	Thr	Leu	Asn	Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Val	Lys	His		
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 340 345 350

Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
 355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala
 370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr
 385 390 395 400

Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
 405 410 415

Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
 420 425 430

Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly
 435 440 445

Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile
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Asn Ala Asp Gly Trp Ala Asn Phe Ser Val Asn Gly Gly Ser Val Ser
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Ile Trp Val Lys Arg
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ccg gat gat ggc acg tta tgg acc aaa gtg gcc aat gaa gcc aac aac 96
 Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn

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Leu	Ser	Ser	Leu	Gly	Ile	Thr	Ala	Leu	Trp	Leu	Pro	Pro	Ala	Tyr	Lys	
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Gly	Thr	Ser	Arg	Ser	Asp	Val	Gly	Tyr	Gly	Val	Tyr	Asp	Leu	Tyr	Asp	
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caa	gtg	tac	gcc	gat	gtc	gtg	ttc	gac	cat	aaa	ggc	ggc	gct	gac	ggc	336
Gln	Val	Tyr	Ala	Asp	Val	Val	Phe	Asp	His	Lys	Gly	Gly	Ala	Asp	Gly	
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Thr	Glu	Trp	Val	Asp	Ala	Val	Glu	Val	Asn	Pro	Ser	Asp	Arg	Asn	Gln	
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gaa	atc	tcg	ggc	acc	tat	caa	atc	caa	gca	tgg	acg	aaa	ttt	gat	ttt	432
Glu	Ile	Ser	Gly	Thr	Tyr	Gln	Ile	Gln	Ala	Trp	Thr	Lys	Phe	Asp	Phe	
	130					135					140					
ccc	ggg	cgg	ggc	aac	acc	tac	tcc	agc	ttt	aag	tgg	cgc	tgg	tac	cat	480
Pro	Gly	Arg	Gly	Asn	Thr	Tyr	Ser	Ser	Phe	Lys	Trp	Arg	Trp	Tyr	His	
145					150					155					160	
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Phe	Asp	Gly	Val	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Leu	Ser	Arg	Ile	Tyr	
				165					170					175		
aaa	ttc	cgc	ggc	atc	ggc	aaa	gcg	tgg	gat	tgg	gaa	gta	gac	acg	gaa	576
Lys	Phe	Arg	Gly	Ile	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Asp	Thr	Glu	
			180					185					190			
aac	gga	aac	tat	gac	tac	tta	atg	tat	gcc	gac	ctt	gat	atg	gat	cat	624
Asn	Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Leu	Asp	Met	Asp	His	
			195				200					205				
ccc	gaa	gtc	gtg	acc	gag	ctg	aaa	aac	tgg	ggg	aaa	tgg	tat	gtc	aac	672
Pro	Glu	Val	Val	Thr	Glu	Leu	Lys	Asn	Trp	Gly	Lys	Trp	Tyr	Val	Asn	
	210					215					220					
aca	acg	aac	att	gat	ggg	ttc	cgg	ctt	gat	gcc	gtc	aag	cat	att	aag	720
Thr	Thr	Asn	Ile	Asp	Gly	Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys	
225					230					235					240	
ttc	agt	ttt	ttt	cct	gat	tgg	ttg	tcg	tat	gtg	cgt	tct	cag	act	ggc	768
Phe	Ser	Phe	Phe	Pro	Asp	Trp	Leu	Ser	Tyr	Val	Arg	Ser	Gln	Thr	Gly	
				245					250					255		

aag ccg cta ttt acc gtc ggg gaa tat tgg agc tat gac atc aac aag Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys 260 265 270	816
ttg cac aat tac att acg aaa aca gac gga acg atg tct ttg ttt gat Leu His Asn Tyr Ile Thr Lys Thr Asp Gly Thr Met Ser Leu Phe Asp 275 280 285	864
gcc ccg tta cac aac aaa ttt tat acc gct tcc aaa tca ggg ggc gca Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Ala 290 295 300	912
ttt gat atg cgc acg tta atg acc aat act ctc atg aaa gat caa ccg Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro 305 310 315 320	960
aca ttg gcc gtc acc ttc gtt gat aat cat gac acc gaa ccc ggc caa Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln 325 330 335	1008
gcg ctg cag tca tgg gtc gac cca tgg ttc aaa ccg ttg gct tac gcc Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala 340 345 350	1056
ttt att cta act cgg cag gaa gga tac ccg tgc gtc ttt tat ggt gac Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp 355 360 365	1104
tat tat ggc att cca caa tat aac att cct tcg ctg aaa agc aaa atc Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile 370 375 380	1152
gat ccg ctc ctc atc gcg cgc agg gat tat gct tac gga acg caa cat Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His 385 390 395 400	1200
gat tat ctt gat cac tcc gac atc atc ggg tgg aca agg gaa ggg ggc Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Gly 405 410 415	1248
act gaa aaa cca gga tcc gga ctg gcc gca ctg atc acc gat ggg ccg Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro 420 425 430	1296
gga gga agc aaa tgg atg tac gtt ggc aaa caa cac gct gga aaa gtg Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val 435 440 445	1344
ttc tat gac ctt acc ggc aac cgg agt gac acc gtc acc atc aac agt Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser 450 455 460	1392
gat gga tgg ggg gaa ttc aaa gtc aat ggc ggt tcg gtt tcg gtt tgg Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp 465 470 475 480	1440

gtt cct aga aaa acg acc gtt tct acc atc gct cgg ccg atc aca acc 1488
 Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Arg Pro Ile Thr Thr
 485 490 495

cga ccg tgg act ggt gaa ttc gtc cgt tgg acc gaa cca cgg ttg gtg 1536
 Arg Pro Trp Thr Gly Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val
 500 505 510

gca tgg cct tga 1548
 Ala Trp Pro
 515

<210> 6
 <211> 515
 <212> PRT
 <213> Bacillus stearothermophilus

<400> 6

Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Leu
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Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn
 20 25 30

Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys
 35 40 45

Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp
 50 55 60

Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr
 65 70 75 80

Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met
 85 90 95

Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly
 100 105 110

Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln
 115 120 125

Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe
 130 135 140

Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His

145					150					155					160
Phe	Asp	Gly	Val	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Leu	Ser	Arg	Ile	Tyr
				165					170					175	
Lys	Phe	Arg	Gly	Ile	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Asp	Thr	Glu
			180					185					190		
Asn	Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Leu	Asp	Met	Asp	His
		195					200					205			
Pro	Glu	Val	Val	Thr	Glu	Leu	Lys	Asn	Trp	Gly	Lys	Trp	Tyr	Val	Asn
	210					215					220				
Thr	Thr	Asn	Ile	Asp	Gly	Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys
225					230					235					240
Phe	Ser	Phe	Phe	Pro	Asp	Trp	Leu	Ser	Tyr	Val	Arg	Ser	Gln	Thr	Gly
				245					250					255	
Lys	Pro	Leu	Phe	Thr	Val	Gly	Glu	Tyr	Trp	Ser	Tyr	Asp	Ile	Asn	Lys
			260					265					270		
Leu	His	Asn	Tyr	Ile	Thr	Lys	Thr	Asp	Gly	Thr	Met	Ser	Leu	Phe	Asp
		275					280					285			
Ala	Pro	Leu	His	Asn	Lys	Phe	Tyr	Thr	Ala	Ser	Lys	Ser	Gly	Gly	Ala
	290					295					300				
Phe	Asp	Met	Arg	Thr	Leu	Met	Thr	Asn	Thr	Leu	Met	Lys	Asp	Gln	Pro
305					310					315					320
Thr	Leu	Ala	Val	Thr	Phe	Val	Asp	Asn	His	Asp	Thr	Glu	Pro	Gly	Gln
				325					330					335	
Ala	Leu	Gln	Ser	Trp	Val	Asp	Pro	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala
			340					345					350		
Phe	Ile	Leu	Thr	Arg	Gln	Glu	Gly	Tyr	Pro	Cys	Val	Phe	Tyr	Gly	Asp
		355					360					365			
Tyr	Tyr	Gly	Ile	Pro	Gln	Tyr	Asn	Ile	Pro	Ser	Leu	Lys	Ser	Lys	Ile
	370					375					380				

Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His
 385 390 395 400

Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Gly
 405 410 415

Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
 420 425 430

Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val
 435 440 445

Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser
 450 455 460

Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp
 465 470 475 480

Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Arg Pro Ile Thr Thr
 485 490 495

Arg Pro Trp Thr Gly Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val
 500 505 510

Ala Trp Pro
 515

<210> 7
 <211> 1920
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (421) .. (1872)

<400> 7
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 gagacggaaa aatcgtctta atgcacgata tttatgcaac gttcgcagat gctgctgaag 120
 agattattaa aaagctgaaa gcaaaaggct atcaattggg aactgtatct cagcttgaag 180
 aagtgaagaa gcagagaggc tattgaataa atgagtagaa gcgccatatc ggcgcttttc 240

ttttggaaga aaatataggg aaaatggtac ttgttaaaaa ttcggaatat ttatacaaca	300
tcatatgttt cacattgaaa ggggaggaga atcatgaaac aacaaaaacg gctttacgcc	360
cgattgctga cgctgttatt tgcgctcatc ttcttgctgc ctcattctgc agcagcggcg	420
gca aat ctt aat ggg acg ctg atg cag tat ttt gaa tgg tac atg ccc Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro 1 5 10 15	468
aat gac ggc caa cat tgg agg cgt ttg caa aac gac tcg gca tat ttg Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu 20 25 30	516
gct gaa cac ggt att act gcc gtc tgg att ccc ccg gca tat aag gga Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly 35 40 45	564
acg agc caa gcg gat gtg ggc tac ggt gct tac gac ctt tat gat tta Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu 50 55 60	612
ggg gag ttt cat caa aaa ggg acg gtt cgg aca aag tac ggc aca aaa Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys 65 70 75 80	660
gga gag ctg caa tct gcg atc aaa agt ctt cat tcc cgc gac att aac Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn 85 90 95	708
gtt tac ggg gat gtg gtc atc aac cac aaa ggc ggc gct gat gcg acc Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr 100 105 110	756
gaa gat gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val 115 120 125	804
att tca gga gaa cac cta att aaa gcc tgg aca cat ttt cat ttt ccg Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro 130 135 140	852
ggg cgc ggc agc aca tac agc gat ttt aaa tgg cat tgg tac cat ttt Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe 145 150 155 160	900
gac gga acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys 165 170 175	948
ttt caa gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn 180 185 190	996
tat gat tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val 195 200 205	1044

gca gca gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa	1092
Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln	
210 215 220	
ttg gac ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt	1140
Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe	
225 230 235 240	
ttg cgg gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg	1188
Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met	
245 250 255	
ttt acg gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac	1236
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn	
260 265 270	
tat ttg aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt	1284
Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu	
275 280 285	
cat tat cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg	1332
His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met	
290 295 300	
agg aaa ttg ctg aac ggt acg gtc gtt tcc aag cat ccg ttg aaa tcg	1380
Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser	
305 310 315 320	
gtt aca ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag	1428
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu	
325 330 335	
tcg act gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc	1476
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu	
340 345 350	
aca agg gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg	1524
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly	
355 360 365	
acg aaa gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att	1572
Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile	
370 375 380	
gaa ccg atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat	1620
Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His	
385 390 395 400	
gat tat ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac	1668
Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp	
405 410 415	
agc tcg gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc	1716
Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro	
420 425 430	

ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca 1764
 Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
 435 440 445

tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg 1812
 Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
 450 455 460

gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat 1860
 Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
 465 470 475 480

gtt caa aga tag aagagcagag aggacggatt tcctgaagga aatccgtttt 1912
 Val Gln Arg

tttattttt 1920

<210> 8
 <211> 483
 <212> PRT
 <213> Bacillus licheniformis

<400> 8

Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
 1 5 10 15

Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu
 20 25 30

Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
 35 40 45

Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
 50 55 60

Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65 70 75 80

Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
 85 90 95

Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
 100 105 110

Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
 115 120 125

Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro
 130 135 140

Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
 145 150 155 160

Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
 165 170 175

Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
 180 185 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
 195 200 205

Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
 210 215 220

Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
 225 230 235 240

Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
 245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
 260 265 270

Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
 275 280 285

His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
 290 295 300

Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser
 305 310 315 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
 325 330 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
 340 345 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
 355 360 365

Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
 370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
 385 390 395 400

Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
 405 410 415

Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
 420 425 430

Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
 435 440 445

Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
 450 455 460

Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
 465 470 475 480

Val Gln Arg

<210> 9
 <211> 2084
 <212> DNA
 <213> Bacillus amyloliquefaciens

<220>
 <221> CDS
 <222> (343)..(1794)

<400> 9
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 ctgaagaagt ggatcgattg tttgagaaaa gaagaagacc ataaaaatac cttgtctgtc 120
 atcagacagg gtatttttta tgctgtccag actgtccgct gtgtaaaaat aaggaataaa 180
 ggggggttgt tattatttta ctgatatgta aaatataatt tgtataagaa aatgagaggg 240
 agaggaaaca tgattcaaaa acgaaagcgg acagtttcgt tcagacttgt gcttatgtgc 300

acgctgttat ttgtcagttt gccgattaca aaaacatcag cc gta aat ggc acg	354
Val Asn Gly Thr	
1	
ctg atg cag tat ttt gaa tgg tat acg ccg aac gac ggc cag cat tgg	402
Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp Gly Gln His Trp	
5 10 15 20	
aaa cga ttg cag aat gat gcg gaa cat tta tcg gat atc gga atc act	450
Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp Ile Gly Ile Thr	
25 30 35	
gcc gtc tgg att cct ccc gca tac aaa gga ttg agc caa tcc gat aac	498
Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser Gln Ser Asp Asn	
40 45 50	
gga tac gga cct tat gat ttg tat gat tta gga gaa ttc cag caa aaa	546
Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Gln Gln Lys	
55 60 65	
ggg acg gtc aga acg aaa tac ggc aca aaa tca gag ctt caa gat gcg	594
Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu Leu Gln Asp Ala	
70 75 80	
atc ggc tca ctg cat tcc cgg aac gtc caa gta tac gga gat gtg gtt	642
Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr Gly Asp Val Val	
85 90 95 100	
ttg aat cat aag gct ggt gct gat gca aca gaa gat gta act gcc gtc	690
Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp Val Thr Ala Val	
105 110 115	
gaa gtc aat ccg gcc aat aga aat cag gaa act tcg gag gaa tat caa	738
Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser Glu Glu Tyr Gln	
120 125 130	
atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt gga aac acg tac	786
Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg Gly Asn Thr Tyr	
135 140 145	
agt gat ttt aaa tgg cat tgg tat cat ttc gac gga gcg gac tgg gat	834
Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly Ala Asp Trp Asp	
150 155 160	
gaa tcc cgg aag atc agc cgc atc ttt aag ttt cgt ggg gaa gga aaa	882
Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg Gly Glu Gly Lys	
165 170 175 180	
gcg tgg gat tgg gaa gta tca agt gaa aac ggc aac tat gac tat tta	930
Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn Tyr Asp Tyr Leu	
185 190 195	
atg tat gct gat gtt gac tac gac cac cct gat gtc gtg gca gag aca	978
Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val Val Ala Glu Thr	
200 205 210	
aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg tca tta gac ggc ttc	1026

Lys	Lys	Trp	Gly	Ile	Trp	Tyr	Ala	Asn	Glu	Leu	Ser	Leu	Asp	Gly	Phe		
		215					220					225					
cgt	att	gat	gcc	gcc	aaa	cat	att	aaa	ttt	tca	ttt	ctg	cgt	gat	tgg		1074
Arg	Ile	Asp	Ala	Ala	Lys	His	Ile	Lys	Phe	Ser	Phe	Leu	Arg	Asp	Trp		
	230					235					240						
ggt	cag	gcg	gtc	aga	cag	gcg	acg	gga	aaa	gaa	atg	ttt	acg	ggt	gcg		1122
Val	Gln	Ala	Val	Arg	Gln	Ala	Thr	Gly	Lys	Glu	Met	Phe	Thr	Val	Ala		
	245				250					255					260		
gag	tat	tgg	cag	aat	aat	gcc	ggg	aaa	ctc	gaa	aac	tac	ttg	aat	aaa		1170
Glu	Tyr	Trp	Gln	Asn	Asn	Ala	Gly	Lys	Leu	Glu	Asn	Tyr	Leu	Asn	Lys		
				265					270					275			
aca	agc	ttt	aat	caa	tcc	gtg	ttt	gat	ggt	ccg	ctt	cat	ttc	aat	tta		1218
Thr	Ser	Phe	Asn	Gln	Ser	Val	Phe	Asp	Val	Pro	Leu	His	Phe	Asn	Leu		
			280					285					290				
cag	gcg	gct	tcc	tca	caa	gga	ggc	gga	tat	gat	atg	agg	cgt	ttg	ctg		1266
Gln	Ala	Ala	Ser	Ser	Gln	Gly	Gly	Gly	Tyr	Asp	Met	Arg	Arg	Leu	Leu		
		295					300					305					
gac	ggt	acc	ggt	gtg	tcc	agg	cat	ccg	gaa	aag	gcg	ggt	aca	ttt	ggt		1314
Asp	Gly	Thr	Val	Val	Ser	Arg	His	Pro	Glu	Lys	Ala	Val	Thr	Phe	Val		
	310					315					320						
gaa	aat	cat	gac	aca	cag	ccg	gga	cag	tca	ttg	gaa	tcg	aca	gtc	caa		1362
Glu	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu	Ser	Thr	Val	Gln		
	325				330					335					340		
act	tgg	ttt	aaa	ccg	ctt	gca	tac	gcc	ttt	att	ttg	aca	aga	gaa	tcc		1410
Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Arg	Glu	Ser		
				345				350						355			
ggt	tat	cct	cag	gtg	ttc	tat	ggg	gat	atg	tac	ggg	aca	aaa	ggg	aca		1458
Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly	Thr	Lys	Gly	Thr		
			360				365					370					
tcg	cca	aag	gaa	att	ccc	tca	ctg	aaa	gat	aat	ata	gag	ccg	att	tta		1506
Ser	Pro	Lys	Glu	Ile	Pro	Ser	Leu	Lys	Asp	Asn	Ile	Glu	Pro	Ile	Leu		
		375				380						385					
aaa	gcg	cgt	aag	gag	tac	gca	tac	ggg	ccc	cag	cac	gat	tat	att	gac		1554
Lys	Ala	Arg	Lys	Glu	Tyr	Ala	Tyr	Gly	Pro	Gln	His	Asp	Tyr	Ile	Asp		
	390					395					400						
cac	ccg	gat	gtg	atc	gga	tgg	acg	agg	gaa	ggt	gac	agc	tcc	gcc	gcc		1602
His	Pro	Asp	Val	Ile	Gly	Trp	Thr	Arg	Glu	Gly	Asp	Ser	Ser	Ala	Ala		
	405				410					415					420		
aaa	tca	ggt	ttg	gcc	gct	tta	atc	acg	gac	gga	ccc	ggc	gga	tca	aag		1650
Lys	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro	Gly	Gly	Ser	Lys		
				425				430						435			
cgg	atg	tat	gcc	ggc	ctg	aaa	aat	gcc	ggc	gag	aca	tgg	tat	gac	ata		1698
Arg	Met	Tyr	Ala	Gly	Leu	Lys	Asn	Ala	Gly	Glu	Thr	Trp	Tyr	Asp	Ile		

440	445	450	
acg ggc aac cgt tca gat act gta aaa atc gga tct gac ggc tgg gga			1746
Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser Asp Gly Trp Gly			
455	460	465	
gag ttt cat gta aac gat ggg tcc gtc tcc att tat gtt cag aaa taa			1794
Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr Val Gln Lys			
470	475	480	
ggtaataaaaa aaacacctcc aagctgagtg cgggtatcag cttggagggtg cggtttatttt			1854
ttcagccgta tgacaagggtc ggcatcaggt gtgacaaata cggtatgctg gctgtcatag			1914
gtgacaaatc cgggtttttgc gccgtttggc tttttcacat gtctgatttt tgtataatca			1974
acaggcacgg agccggaatc tttcgcttg gaaaaataag cggcgatcgt agctgcttcc			2034
aatatggatt gttcatcggg atcgctgctt ttaatcaciaa cgtgggatcc			2084

<210> 10
 <211> 483
 <212> PRT
 <213> *Bacillus amyloliquefaciens*

<400> 10

Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp	
1 5 10 15	
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp	
20 25 30	
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser	
35 40 45	
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu	
50 55 60	
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu	
65 70 75 80	
Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr	
85 90 95	
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp	
100 105 110	
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser	

115					120					125					
Glu	Glu	Tyr	Gln	Ile	Lys	Ala	Trp	Thr	Asp	Phe	Arg	Phe	Pro	Gly	Arg
130						135					140				
Gly	Asn	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	Asp	Gly
145					150					155					160
Ala	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Ile	Ser	Arg	Ile	Phe	Lys	Phe	Arg
				165					170					175	
Gly	Glu	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Ser	Glu	Asn	Gly	Asn
			180					185					190		
Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Val	Asp	Tyr	Asp	His	Pro	Asp	Val
	195						200					205			
Val	Ala	Glu	Thr	Lys	Lys	Trp	Gly	Ile	Trp	Tyr	Ala	Asn	Glu	Leu	Ser
	210					215					220				
Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Ala	Lys	His	Ile	Lys	Phe	Ser	Phe
225					230					235					240
Leu	Arg	Asp	Trp	Val	Gln	Ala	Val	Arg	Gln	Ala	Thr	Gly	Lys	Glu	Met
				245					250					255	
Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asn	Ala	Gly	Lys	Leu	Glu	Asn
			260					265					270		
Tyr	Leu	Asn	Lys	Thr	Ser	Phe	Asn	Gln	Ser	Val	Phe	Asp	Val	Pro	Leu
	275						280					285			
His	Phe	Asn	Leu	Gln	Ala	Ala	Ser	Ser	Gln	Gly	Gly	Gly	Tyr	Asp	Met
	290					295					300				
Arg	Arg	Leu	Leu	Asp	Gly	Thr	Val	Val	Ser	Arg	His	Pro	Glu	Lys	Ala
305					310					315					320
Val	Thr	Phe	Val	Glu	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu
				325					330					335	
Ser	Thr	Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu
			340					345					350		

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
 355 360 365

Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
 370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
 385 390 395 400

Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
 405 410 415

Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
 420 425 430

Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
 435 440 445

Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
 450 455 460

Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr
 465 470 475 480

Val Gln Lys

<210> 11
 <211> 1458
 <212> DNA
 <213> Bacillus sp.

<220>
 <221> CDS
 <222> (1)..(1458)

<400> 11	
cac cat aat ggt acg aac ggc aca atg atg cag tac ttt gaa tgg tat	48
His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr	
1 5 10 15	
cta cca aat gac gga aac cat tgg aat aga tta agg tct gat gca agt	96
Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Ser Asp Ala Ser	
20 25 30	

aac cta aaa gat aaa ggg atc tca gcg gtt tgg att cct cct gca tgg Asn Leu Lys Asp Lys Gly Ile Ser Ala Val Trp Ile Pro Pro Ala Trp 35 40 45	144
aag ggt gcc tct caa aat gat gtg ggg tat ggt gct tat gat ctg tat Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr 50 55 60	192
gat tta gga gaa ttc aat caa aaa gga acc att cgt aca aaa tat gga Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Ile Arg Thr Lys Tyr Gly 65 70 75 80	240
acg cgc aat cag tta caa gct gca gtt aac gcc ttg aaa agt aat gga Thr Arg Asn Gln Leu Gln Ala Ala Val Asn Ala Leu Lys Ser Asn Gly 85 90 95	288
att caa gtg tat ggc gat gtt gta atg aat cat aaa ggg gga gca gac Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp 100 105 110	336
gct acc gaa atg gtt agg gca gtt gaa gta aac ccg aat aat aga aat Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn 115 120 125	384
caa gaa gtg tcc ggt gaa tat aca att gag gct tgg aca aag ttt gac Gln Glu Val Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp 130 135 140	432
ttt cca gga cga ggt aat act cat tca aac ttc aaa tgg aga tgg tat Phe Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr 145 150 155 160	480
cac ttt gat gga gta gat tgg gat cag tca cgt aag ctg aac aat cga His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Lys Leu Asn Asn Arg 165 170 175	528
att tat aaa ttt aga ggt gat gga aaa ggg tgg gat tgg gaa gtc gat Ile Tyr Lys Phe Arg Gly Asp Gly Lys Gly Trp Asp Trp Glu Val Asp 180 185 190	576
aca gaa aac ggt aac tat gat tac cta atg tat gca gat att gac atg Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met 195 200 205	624
gat cac cca gag gta gtg aat gag cta aga aat tgg ggt gtt tgg tat Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr 210 215 220	672
acg aat aca tta ggc ctt gat ggt ttt aga ata gat gca gta aaa cat Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His 225 230 235 240	720
ata aaa tac agc ttt act cgt gat tgg att aat cat gtt aga agt gca Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala 245 250 255	768
act ggc aaa aat atg ttt gcg gtt gcg gaa ttt tgg aaa aat gat tta	816

Thr	Gly	Lys	Asn	Met	Phe	Ala	Val	Ala	Glu	Phe	Trp	Lys	Asn	Asp	Leu		
			260					265					270				
ggg	gct	att	gaa	aac	tat	tta	aac	aaa	aca	aac	tgg	aac	cat	tca	gtc	864	
Gly	Ala	Ile	Glu	Asn	Tyr	Leu	Asn	Lys	Thr	Asn	Trp	Asn	His	Ser	Val		
		275					280					285					
ttt	gat	gtt	ccg	ctg	cac	tat	aac	ctc	tat	aat	gct	tca	aaa	agc	gga	912	
Phe	Asp	Val	Pro	Leu	His	Tyr	Asn	Leu	Tyr	Asn	Ala	Ser	Lys	Ser	Gly		
	290					295				300							
ggg	aat	tat	gat	atg	agg	caa	ata	ttt	aat	ggg	aca	gtc	gtg	caa	aga	960	
Gly	Asn	Tyr	Asp	Met	Arg	Gln	Ile	Phe	Asn	Gly	Thr	Val	Val	Gln	Arg		
305					310				315						320		
cat	cca	atg	cat	gct	gtt	aca	ttt	gtt	gat	aat	cat	gat	tcg	caa	cct	1008	
His	Pro	Met	His	Ala	Val	Thr	Phe	Val	Asp	Asn	His	Asp	Ser	Gln	Pro		
				325					330					335			
gaa	gaa	gct	tta	gag	tct	ttt	gtt	gaa	gaa	tgg	ttc	aaa	cca	tta	gcg	1056	
Glu	Glu	Ala	Leu	Glu	Ser	Phe	Val	Glu	Glu	Trp	Phe	Lys	Pro	Leu	Ala		
			340					345					350				
tat	gct	ttg	aca	tta	aca	cgt	gaa	caa	ggc	tac	cct	tct	gta	ttt	tat	1104	
Tyr	Ala	Leu	Thr	Leu	Thr	Arg	Glu	Gln	Gly	Tyr	Pro	Ser	Val	Phe	Tyr		
		355				360					365						
gga	gat	tat	tat	ggc	att	cca	acg	cat	ggg	gta	cca	gcg	atg	aaa	tcg	1152	
Gly	Asp	Tyr	Tyr	Gly	Ile	Pro	Thr	His	Gly	Val	Pro	Ala	Met	Lys	Ser		
	370				375						380						
aaa	att	gac	ccg	att	cta	gaa	gcg	cgt	caa	aag	tat	gca	tat	gga	aga	1200	
Lys	Ile	Asp	Pro	Ile	Leu	Glu	Ala	Arg	Gln	Lys	Tyr	Ala	Tyr	Gly	Arg		
385					390				395						400		
caa	aat	gac	tac	tta	gac	cat	cat	aat	atc	atc	ggg	tgg	aca	cgt	gaa	1248	
Gln	Asn	Asp	Tyr	Leu	Asp	His	His	Asn	Ile	Ile	Gly	Trp	Thr	Arg	Glu		
				405					410					415			
ggg	aat	aca	gca	cac	ccc	aac	tcc	ggg	tta	gct	act	atc	atg	tcc	gat	1296	
Gly	Asn	Thr	Ala	His	Pro	Asn	Ser	Gly	Leu	Ala	Thr	Ile	Met	Ser	Asp		
			420					425					430				
ggg	gca	gga	gga	aat	aag	tgg	atg	ttt	gtt	ggg	cgt	aat	aaa	gct	ggg	1344	
Gly	Ala	Gly	Gly	Asn	Lys	Trp	Met	Phe	Val	Gly	Arg	Asn	Lys	Ala	Gly		
		435					440					445					
caa	gtt	tgg	acc	gat	atc	act	gga	aat	cgt	gca	ggg	act	gtt	acg	att	1392	
Gln	Val	Trp	Thr	Asp	Ile	Thr	Gly	Asn	Arg	Ala	Gly	Thr	Val	Thr	Ile		
		450				455					460						
aat	gct	gat	gga	tgg	ggg	aat	ttt	tct	gta	aat	gga	gga	tca	gtt	tct	1440	
Asn	Ala	Asp	Gly	Trp	Gly	Asn	Phe	Ser	Val	Asn	Gly	Gly	Ser	Val	Ser		
465					470					475					480		
att	tgg	gta	aac	aaa	taa											1458	
Ile	Trp	Val	Asn	Lys													

485

<210> 12
 <211> 485
 <212> PRT
 <213> Bacillus sp.

<400> 12

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
 1 5 10 15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Ser Asp Ala Ser
 20 25 30

Asn Leu Lys Asp Lys Gly Ile Ser Ala Val Trp Ile Pro Pro Ala Trp
 35 40 45

Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
 50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Ile Arg Thr Lys Tyr Gly
 65 70 75 80

Thr Arg Asn Gln Leu Gln Ala Ala Val Asn Ala Leu Lys Ser Asn Gly
 85 90 95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
 100 105 110

Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn
 115 120 125

Gln Glu Val Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
 130 135 140

Phe Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr
 145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Lys Leu Asn Asn Arg
 165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Gly Trp Asp Trp Glu Val Asp
 180 185 190

Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Ala Gly Gly Asn Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly
435 440 445

Gln Val Trp Thr Asp Ile Thr Gly Asn Arg Ala Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Ile Trp Val Asn Lys
485

<210> 13
<211> 197
<212> PRT
<213> Bacillus sp 707

<400> 13

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly
1 5 10 15

Gly Asn Tyr Asp Met Arg Asn Ile Phe Asn Gly Thr Val Val Gln Arg
20 25 30

His Pro Ser His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
35 40 45

Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala
50 55 60

Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
65 70 75 80

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Arg Ser
85 90 95

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Lys
100 105 110

Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
115 120 125

Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
 130 135 140

Gly Ala Gly Gly Ser Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly
 145 150 155 160

Gln Val Trp Ser Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
 165 170 175

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
 180 185 190

Ile Trp Val Asn Lys
 195

<210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer 22149

<400> 14
 cgattgctga cgctgttatt tgcg 24

<210> 15
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer 24814

<400> 15
 gatcaccgc gataccgtc 19

<210> 16
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer # 24

<400> 16
 gaatgtatgt cggccggcaa aacgccggtg a 31

<210> 17
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer # 27

 <400> 17
 gccgccgctg ctgcagaatg aggcagcaag 30

 <210> 18
 <211> 48
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer # 312

 <400> 18
 cccgaaagct gaaccgcatt tataggtttc aagggaagac ttgggatt 48

 <210> 19
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer 290

 <400> 19
 aggatgggtca taatcaaagt cgg 23

 <210> 20
 <211> 52
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer #313

 <400> 20
 ccgactttga ttatgaccat cctgttggtc tagcagagat taagagatgg gg 52

 <210> 21
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer # 314

<400> 21
cgacaatgtc atggtgggtcg aaaaaatcat gctgtgctcc gtacg 45

<210> 22
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer #296

<400> 22
tttcgaccac catgacattg tcg 23

<210> 23
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer #305

<400> 23
tatagatgcg gttcagcttt cggg 24

<210> 24
<211> 1650
<212> DNA
<213> Bacillus sp.

<400> 24
cttgaatcat tatttaaagc tggttatgat atatgtaagc gttatcatta aaaggaggta 60
tttgatgaaa agatgggtag tagcaatgct ggcagtgtta tttttatttc cttcggtagt 120
agttgcagat ggcttgaatg gaacgatgat gcagtattat gagtggcatc tagagaatga 180
tgggcaacac tggaatcggg tgcgatgatga tgccgaagct ttaagtaatg cgggtattac 240
agctatttgg atacccccag cctacaaagg aaatagtcag gctgatgttg ggtatggtgc 300
atacgacctt tatgatttag gggagttaa tcaaaaagg accgttcgaa cgaaatacgg 360
gacaaaggct cagcttgagc gagctatagg gtccctaaag tcgaatgata tcaatgttta 420
tggggatgtc gtaatgaatc ataaattagg agctgatttc acggaggcag tgcaagctgt 480
tcaagtaa at ccttcgaacc gttggcagga tatttcaggt gtctacacga ttgatgcatg 540
gacgggattt gactttccag ggcgcaacaa tgccatttcc gattttaaat ggagatgggt 600
ccattttaat ggcgttgact gggatcaacg ctatcaagaa aaccatcttt ttcgctttgc 660
aaatacgaac tggaactggc gagtggatga agagaatggg aattatgact atttattagg 720

atcgaacatt gacttttagcc acccagaggt tcaagaggaa ttaaaggatt gggggagctg 780
 gtttacggat gagctagatt tagatgggta tcgattggat gctattaagc atattccatt 840
 ctggtatacg tcagattggg ttaggcatca gcgaagtga gacagaccaag atttatttgt 900
 cgtaggggag tattggaagg atgacgtagg tgctctcgaa ttttatttag atgaaatgaa 960
 ttgggagatg tctctattcg atgttccgct caattataat ttttaccggg cttcaaagca 1020
 aggcggaagc tatgatatgc gtaatatattt acgaggatct ttagtagaag cacatccgat 1080
 tcatgcagtt acgtttgttg ataatcatga tactcagcca ggagagtcac tagaatcatg 1140
 ggtcgctgat tggtttaagc cacttgctta tgcgacaatc ttgacgcgtg aaggtgggta 1200
 tccaaatgta ttttacggtg actactatgg gattcctaac gataacattt cagctaagaa 1260
 ggatatgatt gatgagttgc ttgatgcacg tcaaaattac gcatatggca cacaacatga 1320
 ctattttgat cattgggata tcgttggatg gacaagagaa ggtacatcct cacgtcctaa 1380
 ttcgggtctt gctactatta tgtccaatgg tcctggagga tcaaaatgga tgtacgtagg 1440
 acagcaacat gcaggacaaa cgtggacaga tttaactggc aatcacgcgg cgtcgggttac 1500
 gattaatggt gatggctggg gcgaattctt tacaaatgga ggatctgtat ccgtgtatgt 1560
 gaaccaataa taaaaagcct tgagaaggga ttcttcccta actcaaggct ttctttatgt 1620
 cgttttagctc aacgcttcta cgaagcttta 1650

<210> 25
 <211> 501
 <212> PRT
 <213> Bacillus sp.

<400> 25

Met Lys Arg Trp Val Val Ala Met Leu Ala Val Leu Phe Leu Phe Pro
 1 5 10 15

Ser Val Val Val Ala Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr
 20 25 30

Glu Trp His Leu Glu Asn Asp Gly Gln His Trp Asn Arg Leu His Asp
 35 40 45

Asp Ala Glu Ala Leu Ser Asn Ala Gly Ile Thr Ala Ile Trp Ile Pro
 50 55 60

Pro Ala Tyr Lys Gly Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr
65 70 75 80

Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr
85 90 95

Lys Tyr Gly Thr Lys Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys
100 105 110

Ser Asn Asp Ile Asn Val Tyr Gly Asp Val Val Met Asn His Lys Leu
115 120 125

Gly Ala Asp Phe Thr Glu Ala Val Gln Ala Val Gln Val Asn Pro Ser
130 135 140

Asn Arg Trp Gln Asp Ile Ser Gly Val Tyr Thr Ile Asp Ala Trp Thr
145 150 155 160

Gly Phe Asp Phe Pro Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp
165 170 175

Arg Trp Phe His Phe Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu
180 185 190

Asn His Leu Phe Arg Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp
195 200 205

Glu Glu Asn Gly Asn Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe
210 215 220

Ser His Pro Glu Val Gln Glu Glu Leu Lys Asp Trp Gly Ser Trp Phe
225 230 235 240

Thr Asp Glu Leu Asp Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His
245 250 255

Ile Pro Phe Trp Tyr Thr Ser Asp Trp Val Arg His Gln Arg Ser Glu
260 265 270

Ala Asp Gln Asp Leu Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val
275 280 285

Gly Ala Leu Glu Phe Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu

290		295		300
Phe Asp Val Pro Leu Asn Tyr Asn Phe Tyr Arg Ala Ser Lys Gln Gly				
305		310	315	320
Gly Ser Tyr Asp Met Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala				
	325		330	335
His Pro Ile His Ala Val Thr Phe Val Asp Asn His Asp Thr Gln Pro				
	340		345	350
Gly Glu Ser Leu Glu Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala				
	355		360	365
Tyr Ala Thr Ile Leu Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr				
	370		375	380
Gly Asp Tyr Tyr Gly Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp				
385		390	395	400
Met Ile Asp Glu Leu Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr				
	405		410	415
Gln His Asp Tyr Phe Asp His Trp Asp Ile Val Gly Trp Thr Arg Glu				
	420		425	430
Gly Thr Ser Ser Arg Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn				
	435		440	445
Gly Pro Gly Gly Ser Lys Trp Met Tyr Val Gly Gln Gln His Ala Gly				
	450		455	460
Gln Thr Trp Thr Asp Leu Thr Gly Asn His Ala Ala Ser Val Thr Ile				
465		470	475	480
Asn Gly Asp Gly Trp Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser				
	485		490	495
Val Tyr Val Asn Gln				
	500			

<210> 26
 <211> 1745

<212> DNA
 <213> Bacillus sp.

<220>
 <221> CDS
 <222> (190)..(1692)

<220>
 <221> sig_peptide
 <222> (190)..(253)

<220>
 <221> mat_peptide
 <222> (253)..()

<400> 26
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 actagcactc ttcagggact aaaccacctt ttttccaaaa atgacatcat ataaacaaat 120
 ttgtctacca atcactatct aaagctgttt atgatatatg taagcgttat cattaaaagg 180
 aggtatcttg atg aga aga tgg gta gta gca atg ttg gca gtg tta ttt tta 231
 Met Arg Arg Trp Val Val Ala Met Leu Ala Val Leu Phe Leu
 -20 -15 -10
 ttt cct tcg gta gta gtt gca gat gga ttg aac ggt acg atg atg cag 279
 Phe Pro Ser Val Val Val Ala Asp Gly Leu Asn Gly Thr Met Met Gln
 -5 -1 1 5
 tat tat gag tgg cat ttg gaa aac gac ggg cag cat tgg aat cgg ttg 327
 Tyr Tyr Glu Trp His Leu Glu Asn Asp Gly Gln His Trp Asn Arg Leu
 10 15 20 25
 cac gat gat gcc gca gct ttg agt gat gct ggt att aca gct att tgg 375
 His Asp Asp Ala Ala Ala Leu Ser Asp Ala Gly Ile Thr Ala Ile Trp
 30 35 40
 att ccg cca gcc tac aaa ggt aat agt cag gcg gat gtt ggg tac ggt 423
 Ile Pro Pro Ala Tyr Lys Gly Asn Ser Gln Ala Asp Val Gly Tyr Gly
 45 50 55
 gca tac gat ctt tat gat tta gga gag ttc aat caa aag ggt act gtt 471
 Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val
 60 65 70
 cga acg aaa tac gga act aag gca cag ctt gaa cga gct att ggg tcc 519
 Arg Thr Lys Tyr Gly Thr Lys Ala Gln Leu Glu Arg Ala Ile Gly Ser
 75 80 85
 ctt aaa tct aat gat atc aat gta tac gga gat gtc gtg atg aat cat 567
 Leu Lys Ser Asn Asp Ile Asn Val Tyr Gly Asp Val Val Met Asn His
 90 95 100 105
 aaa atg gga gct gat ttt acg gag gca gtg caa gct gtt caa gta aat 615
 Lys Met Gly Ala Asp Phe Thr Glu Ala Val Gln Ala Val Gln Val Asn

110	115	120	
cca acg aat cgt tgg cag gat att tca ggt gcc tac acg att gat gcg Pro Thr Asn Arg Trp Gln Asp Ile Ser Gly Ala Tyr Thr Ile Asp Ala 125 130 135			663
tgg acg ggt ttc gac ttt tca ggg cgt aac aac gcc tat tca gat ttt Trp Thr Gly Phe Asp Phe Ser Gly Arg Asn Asn Ala Tyr Ser Asp Phe 140 145 150			711
aag tgg aga tgg ttc cat ttt aat ggt gtt gac tgg gat cag cgc tat Lys Trp Arg Trp Phe His Phe Asn Gly Val Asp Trp Asp Gln Arg Tyr 155 160 165			759
caa gaa aat cat att ttc cgc ttt gca aat acg aac tgg aac tgg cga Gln Glu Asn His Ile Phe Arg Phe Ala Asn Thr Asn Trp Asn Trp Arg 170 175 180 185			807
gtg gat gaa gag aac ggt aat tat gat tac ctg tta gga tcg aat atc Val Asp Glu Glu Asn Gly Asn Tyr Asp Tyr Leu Leu Gly Ser Asn Ile 190 195 200			855
gac ttt agt cat cca gaa gta caa gat gag ttg aag gat tgg ggt agc Asp Phe Ser His Pro Glu Val Gln Asp Glu Leu Lys Asp Trp Gly Ser 205 210 215			903
tgg ttt acc gat gag tta gat ttg gat ggt tat cgt tta gat gct att Trp Phe Thr Asp Glu Leu Asp Leu Asp Gly Tyr Arg Leu Asp Ala Ile 220 225 230			951
aaa cat att cca ttc tgg tat aca tct gat tgg gtt cgg cat cag cgc Lys His Ile Pro Phe Trp Tyr Thr Ser Asp Trp Val Arg His Gln Arg 235 240 245			999
aac gaa gca gat caa gat tta ttt gtc gta ggg gaa tat tgg aag gat Asn Glu Ala Asp Gln Asp Leu Phe Val Val Gly Glu Tyr Trp Lys Asp 250 255 260 265			1047
gac gta ggt gct ctc gaa ttt tat tta gat gaa atg aat tgg gag atg Asp Val Gly Ala Leu Glu Phe Tyr Leu Asp Glu Met Asn Trp Glu Met 270 275 280			1095
tct cta ttc gat gtt cca ctt aat tat aat ttt tac cgg gct tca caa Ser Leu Phe Asp Val Pro Leu Asn Tyr Asn Phe Tyr Arg Ala Ser Gln 285 290 295			1143
caa ggt gga agc tat gat atg cgt aat att tta cga gga tct tta gta Gln Gly Gly Ser Tyr Asp Met Arg Asn Ile Leu Arg Gly Ser Leu Val 300 305 310			1191
gaa gcg cat ccg atg cat gca gtt acg ttt gtt gat aat cat gat act Glu Ala His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Thr 315 320 325			1239
cag cca ggg gag tca tta gag tca tgg gtt gct gat tgg ttt aag cca Gln Pro Gly Glu Ser Leu Glu Ser Trp Val Ala Asp Trp Phe Lys Pro 330 335 340 345			1287

ctt gct tat gcg aca att ttg acg cgt gaa ggt ggt tat cca aat gta	1335
Leu Ala Tyr Ala Thr Ile Leu Thr Arg Glu Gly Gly Tyr Pro Asn Val	
350 355 360	

ttt tac ggt gat tac tat ggg att cct aac gat aac att tca gct aaa	1383
Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro Asn Asp Asn Ile Ser Ala Lys	
365 370 375	

aaa gat atg att gat gag ctg ctt gat gca cgt caa aat tac gca tat	1431
Lys Asp Met Ile Asp Glu Leu Leu Asp Ala Arg Gln Asn Tyr Ala Tyr	
380 385 390	

ggc acg cag cat gac tat ttt gat cat tgg gat gtt gta gga tgg act	1479
Gly Thr Gln His Asp Tyr Phe Asp His Trp Asp Val Val Gly Trp Thr	
395 400 405	

agg gaa gga tct tcc tcc aga cct aat tca ggc ctt gcg act att atg	1527
Arg Glu Gly Ser Ser Ser Arg Pro Asn Ser Gly Leu Ala Thr Ile Met	
410 415 420 425	

tcg aat gga cct ggt ggt tcc aag tgg atg tat gta gga cgt cag aat	1575
Ser Asn Gly Pro Gly Gly Ser Lys Trp Met Tyr Val Gly Arg Gln Asn	
430 435 440	

gca gga caa aca tgg aca gat tta act ggt aat aac gga gcg tcc gtt	1623
Ala Gly Gln Thr Trp Thr Asp Leu Thr Gly Asn Asn Gly Ala Ser Val	
445 450 455	

aca att aat ggc gat gga tgg ggc gaa ttc ttt acg aat gga gga tct	1671
Thr Ile Asn Gly Asp Gly Trp Gly Glu Phe Phe Thr Asn Gly Gly Ser	
460 465 470	

gta tcc gtg tac gtg aac caa taacaaaaag ccttgagaag ggattcctcc	1722
Val Ser Val Tyr Val Asn Gln	
475 480	

ctaactcaag gcttttcttta tgt	1745
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<210> 27
 <211> 501
 <212> PRT
 <213> Bacillus sp.

<400> 27

Met Arg Arg Trp Val Val Ala Met Leu Ala Val Leu Phe Leu Phe Pro
-20 -15 -10

Ser Val Val Val Ala Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr
-5 -1 1 5 10

Glu Trp His Leu Glu Asn Asp Gly Gln His Trp Asn Arg Leu His Asp
15 20 25

Asp Ala Ala Ala Leu Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro
 30 35 40

Pro Ala Tyr Lys Gly Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr
 45 50 55

Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr
 60 65 70 75

Lys Tyr Gly Thr Lys Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys
 80 85 90

Ser Asn Asp Ile Asn Val Tyr Gly Asp Val Val Met Asn His Lys Met
 95 100 105

Gly Ala Asp Phe Thr Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr
 110 115 120

Asn Arg Trp Gln Asp Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr
 125 130 135

Gly Phe Asp Phe Ser Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp
 140 145 150 155

Arg Trp Phe His Phe Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu
 160 165 170

Asn His Ile Phe Arg Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp
 175 180 185

Glu Glu Asn Gly Asn Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe
 190 195 200

Ser His Pro Glu Val Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe
 205 210 215

Thr Asp Glu Leu Asp Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His
 220 225 230 235

Ile Pro Phe Trp Tyr Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu
 240 245 250

Ala Asp Gln Asp Leu Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val
 255 260 265

Gly Ala Leu Glu Phe Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu
 270 275 280

Phe Asp Val Pro Leu Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly
 285 290 295

Gly Ser Tyr Asp Met Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala
 300 305 310 315

His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Thr Gln Pro
 320 325 330

Gly Glu Ser Leu Glu Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala
 335 340 345

Tyr Ala Thr Ile Leu Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr
 350 355 360

Gly Asp Tyr Tyr Gly Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp
 365 370 375

Met Ile Asp Glu Leu Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr
 380 385 390 395

Gln His Asp Tyr Phe Asp His Trp Asp Val Val Gly Trp Thr Arg Glu
 400 405 410

Gly Ser Ser Ser Arg Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn
 415 420 425

Gly Pro Gly Gly Ser Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly
 430 435 440

Gln Thr Trp Thr Asp Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile
 445 450 455

Asn Gly Asp Gly Trp Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser
 460 465 470 475

Val Tyr Val Asn Gln
480

<210> 28
<211> 501
<212> PRT
<213> Bacillus sp

<400> 28

Met Arg Arg Trp Val Val Ala Met Leu Ala Val Leu Phe Leu Phe Pro
1 5 10 15

Ser Val Val Val Ala Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr
20 25 30

Glu Trp His Leu Glu Asn Asp Gly Gln His Trp Asn Arg Leu His Asp
35 40 45

Asp Ala Ala Ala Leu Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro
50 55 60

Pro Ala Tyr Lys Gly Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr
65 70 75 80

Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr
85 90 95

Lys Tyr Gly Thr Lys Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys
100 105 110

Ser Asn Asp Ile Asn Val Tyr Gly Asp Val Val Met Asn His Lys Met
115 120 125

Gly Ala Asp Phe Thr Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr
130 135 140

Asn Arg Trp Gln Asp Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr
145 150 155 160

Gly Phe Asp Phe Ser Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp
165 170 175

Arg Trp Phe His Phe Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu
180 185 190

Asn His Ile Phe Arg Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp
 195 200 205

Glu Glu Asn Gly Asn Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe
 210 215 220

Ser His Pro Glu Val Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe
 225 230 235 240

Thr Asp Glu Leu Asp Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His
 245 250 255

Ile Pro Phe Trp Tyr Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu
 260 265 270

Ala Asp Gln Asp Leu Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val
 275 280 285

Gly Ala Leu Glu Phe Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu
 290 295 300

Phe Asp Val Pro Leu Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly
 305 310 315 320

Gly Ser Tyr Asp Met Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala
 325 330 335

His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Thr Gln Pro
 340 345 350

Gly Glu Ser Leu Glu Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala
 355 360 365

Tyr Ala Thr Ile Leu Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr
 370 375 380

Gly Asp Tyr Tyr Gly Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp
 385 390 395 400

Met Ile Asp Glu Leu Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr
 405 410 415

Gln His Asp Tyr Phe Asp His Trp Asp Val Val Gly Trp Thr Arg Glu
420 425 430

Gly Ser Ser Ser Arg Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn
435 440 445

Gly Pro Gly Gly Ser Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly
450 455 460

Gln Thr Trp Thr Asp Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile
465 470 475 480

Asn Gly Asp Gly Trp Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser
485 490 495

Val Tyr Val Asn Gln
500

<210> 29
<211> 1920
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (421)..(1872)

<400> 29
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gagacggaaa aatcgtctta atgcacgata tttatgcaac gttcgcagat gctgctgaag 120
agattattaa aaagctgaaa gcaaaaggct atcaattggg aactgtatct cagcttgaag 180
aagtgaagaa gcagagaggc tattgaataa atgagtagaa gcgccatatc ggcgcttttc 240
ttttggaaga aaatataggg aaaatggtac ttgttaaaaa ttcggaatat ttatacaaca 300
tcatatgttt cacattgaaa ggggaggaga atcatgaaac aacaaaaacg gctttacgcc 360
cgattgctga cgctgttatt tgcgctcatc ttcttgctgc ctcatcttgc agcagcggcg 420
gca aat ctt aat ggg acg ctg atg cag tat ttt gaa tgg tac atg ccc 468
Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
1 5 10 15
aat gac ggc caa cat tgg agg cgt ttg caa aac gac tcg gca tat ttg 516
Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu
20 25 30

gct gaa cac ggt att act gcc gtc tgg att ccc ccg gca tat aag gga Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly 35 40 45	564
acg agc caa gcg gat gtg ggc tac ggt gct tac gac ctt tat gat tta Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu 50 55 60	612
ggg gag ttt cat caa aaa ggg acg gtt cgg aca aag tac ggc aca aaa Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys 65 70 75 80	660
gga gag ctg caa tct gcg atc aaa agt ctt cat tcc cgc gac att aac Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn 85 90 95	708
gtt tac ggg gat gtg gtc atc aac cac aaa ggc ggc gct gat gcg acc Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr 100 105 110	756
gaa gat gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val 115 120 125	804
att tca gga gaa cac cta att aaa gcc tgg aca cat ttt cat ttt ccg Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro 130 135 140	852
ggg cgc ggc agc aca tac agc gat ttt aaa tgg cat tgg tac cat ttt Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe 145 150 155 160	900
gac gga acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys 165 170 175	948
ttt caa gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn 180 185 190	996
tat gat tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val 195 200 205	1044
gca gca gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln 210 215 220	1092
ttg gac ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe 225 230 235 240	1140
ttg cgg gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met 245 250 255	1188

ttt acg gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac	1236
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn	
260 265 270	
tat ttg aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt	1284
Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu	
275 280 285	
cat tat cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg	1332
His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met	
290 295 300	
agg aaa ttg ctg aac ggt acg gtc gtt tcc aag cat ccg ttg aaa tcg	1380
Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser	
305 310 315 320	
gtt aca ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag	1428
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu	
325 330 335	
tcg act gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc	1476
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu	
340 345 350	
aca agg gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg	1524
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly	
355 360 365	
acg aaa gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att	1572
Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile	
370 375 380	
gaa ccg atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat	1620
Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His	
385 390 395 400	
gat tat ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac	1668
Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp	
405 410 415	
agc tcg gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc	1716
Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro	
420 425 430	
ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca	1764
Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr	
435 440 445	
tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg	1812
Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser	
450 455 460	
gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat	1860
Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr	
465 470 475 480	
gtt caa aga tag aagagcagag aggacggatt tcctgaagga aatccgtttt	1912

Val Gln Arg

tttatttt

1920

<210> 30
<211> 483
<212> PRT
<213> Bacillus licheniformis

<400> 30

Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
1 5 10 15

Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu
20 25 30

Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60

Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
85 90 95

Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
100 105 110

Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
115 120 125

Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro
130 135 140

Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
145 150 155 160

Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
165 170 175

Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
180 185 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
195 200 205

Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
210 215 220

Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
225 230 235 240

Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
260 265 270

Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
275 280 285

His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
290 295 300

Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser
305 310 315 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
325 330 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
340 345 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
355 360 365

Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
385 390 395 400

Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp

405

410

415

Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
420 425 430

Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
435 440 445

Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
450 455 460

Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
465 470 475 480

Val Gln Arg